Access	DB#	

## SEARCH REQUEST FORM

### Scientific and Technical Information Center

Requester's Full Name:		Examiner#:	Date:		
Art Unit: Phor	ne Number 30	Serial Number:			
Mail Box and Bldg/Room Local	tion:d	Results Format Preferred (circle):	PAPER DISK E-MAIL		
If more than one search is su					
Please provide a detailed statement of Include the elected species or structure utility of the invention. Define any ter known, Please attach a copy of the coy	es, keywords, synonyms, a ms that may have a specia	acronyms, and registry numbers, and early meaning. Give examples or relevant	ombine with the concept or		
Title of invention:					
Inventors (please provide full names):					
Earliest Priority Filing Date:	•				
*For Sequence Searches Only* Please in appropriete serial number.	clude all pertinent informat	ton (parent, child, divisional, or issued pa	tent numbers) along with the		
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TAFF USE ONLY	Type of Search	Vendors and cost when			
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archer Phone #: 22504	AA Sequence (#)	•			
ercher Location:	Structure (#)				
ie Scarcher Picked Up: 370 05	Bibliographic	Dr.Link			
ite Completed: 3)405	Litigation				
archer Prep - Review Time:	Fulltext				
crical Prep in me: K .	Patent Family				
nine Time	Other	Other (specify)			

PTO-1590 (8-01)



# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 146331

TO: Ilia Ouspenski Location: 3d74 / 3c70

Wednesday, March 02, 2005

Art Unit: 1644 Phone: 272-2920

**Serial Number: 10 / 032214** 

From: Jan Delaval

Location: Biotech-Chem Library

**Rem 1a51** 

Phone: 272-2504

jan.delaval@uspto.gov

Search Notes	
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From:

Sent:

Ouspenski, Ilia Tuesday, March 01, 2005 9:21 AM Delaval, Jan

To:

Subject:

seq search for 10/032,214

Dear jan,

please search amino acid seq id no:278 for 10032214.

thanks,

ilia

ILIA OUSPENSKI, Ph.D. Examiner Art Unit 1644 Phone:571-272-2920 **REM 3D74** Mailstop 3c70

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A,Title: Structure, expression, and T cell costimulatory activity of the murine homol A,Reference number: S17291; MUID:91341422; PMID:1714935

A,Accession: S17291

A;Molecule type: mRNA
A;Residues: 1-274,'R',279-309 <FRE>
A;Cross references: EMBL;X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
R;Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A;Title: Identification of an alternatively spliced form of the murine homologue of B,Accession: 149521; MUID:94220123; PMID:7513163
A;Accession: 149521
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-143,238-274,'R',279-309 <RE2>
A;Cross-references: GB:D16220; NID:g505178; PIDN:BAA03748.1; PID:g994769
C;Genetics:
Science 262, 909-911, 1933

A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell prolif; Reference number: A48754; MUID:94053735; PMID:7694363

A;Accession: A48754

A;Status: preliminary

A;Molecule type: mMNA

A;Residues: 1-329 <FRES

A;Cross-references: UNIPROT:P42081; GB:L25259; NID:9416368; PIDN:AAA58389.1; PID:9416368

A;Note: it is uncertain whether Met-1 or Met-7 is the initiator

A;Note: it is uncertain whether Met-1 or Met-7 is the initiator

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A;Inttons: 37/1; 143/1; 237/1; 275/1
A;Inttons: 37/1; 143/1; 237/1; 275/1
C;Superfamily: B-lymphocyte restricted
C;Keywords: alternative splicing
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A; Residues: C; Comment: Tl
C; Genetics:
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-329 <AZU>
A;Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839
C;Genetics:
A;Genetics: CD28LG2
A;Gross-references: GD8:433597; OMIM:601020
A;Map position: 3q13.3-3q21
C;Superfamily: B7-2 antigen
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD86 spliced variant CD86 deltaTM isoform ("Species: Homo sapiens (man) C;Date: 30-Jun-2001 #sequence_revision 30-C;Accession: JC7604 R;Magistrelli, G.; Caron, G.; Gauchat, J.F
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                                                                                                                                                                                                                                                                                 A;Gene: cd86deltaTM
C;Superfamily: B-lyn
C;Keywords: immune 1
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Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A;Title: Identification of an alternatively spliced variant
A;Reference number: JC7604; MUID:21092744; PMID:11162656
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Homo sapiens (man);
Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 18-Nov-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                   Keywords: immune response
                                                                                                                                                                                                                                                                                                      Superfamily: B-lymphocyte restricted antigen
                                                                                                                                                                                                                                                                                                                                                              Comment: This CD86 variant expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 LAEVTLSVKADFPTPSISDFEIPTSNIR-----RIICSTSGGFPEP-HLSWLENGEELNA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 FFQLLVLAGLSHFCSGVIHVTKEVKEVATLSC----GHNVSVEBLAQTRIYWQKEKKWVL
                                       60 NEVYLGKEKFDSVHSKYMGRTSFD-SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIH
                                                                                                                                                           19 FFQLLVLAGLSHFCSGVIHVTKEVKEVATLSC----GHNVSVEELAQTRIYWQKEKKMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 NEVYLGKEKFDSVHSKYMGRTSFD-SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 TMM----SGDMNIWPEYKURTIFDITNULSIVILALRPSDEGTYECVVLKYEKDAFKREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 FVMAFLLSG-----AAPLKIQAYFNETADLPCQFANSQNQSLSELV---VFWQDQENLVL
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                                                                                                                                                                                                                                                                                                                                                                                     1-275 <MAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 78; Conserv
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNSTIEYDGIMQKSODNVTELYDVSISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIE
                                                                           TMM----SGDMNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREH
                                                                                                               FVMAFILSG----AAPLKIQAYFNETADLPCQFANSQNQSLSELV---VFWQDQENLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNERL-RRESV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEDPQPPPDHI--PW---ITAVLPTVIICVMVFCLILWKWKKKRPRNSYKCGTNTMERE
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  LAEVTLSVKADFPTPSISDFEIPTSNIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMNSELSVLANFSQPEI----VPISNITENVYINLTCSSIHGYPEPKKMSVL----LRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTTV-----SQDPETELYAVSSKLDF---NMTTNHSFMCLIKYGHLR-VNQTFNWN 232
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                    12.1%; Score 186.5; DB 2; 26.0%; Pred. No. 4.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; Score 201.5; DB 1; 25.1%; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                   Mismatches
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-RIICSTSGGFPEP-HLSWLENGEELNA 184
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                                                                                                                                                                                                                                         Length
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